



(B)

Wed Nov 21 09:31:35 2001 [BLASTP 2.2.1 [Jul-12-2001], NCBI]
home/ruby/va/Molbio/carpanda/tempblast/pl.DNA35680 (1003 aa)

Sequences producing High-scoring Segment Pairs:				Score	Match
Pct	E-val				
1	P_AAB65162	Human PRO290 (UNQ253) protein sequence SE	5247	1003	
100	0.0				
2	P_AAB24058	Human PRO290 protein sequence SEQ ID NO:7	5247	1003	
100	0.0				
3	P_AAY66639	Membrane-bound protein PRO290 - Homo sapi	5235	1003	
100	0.0				
4	P_AAB80418	Gene #4 associated peptide #1 - Homo sapi	5206	1003	
97	0.0				
5	P_AAB80374	Secreted protein encoded by gene #4 - Hom	4810	927	
97	0.0				

>1 P_AAB65162 Human PRO290 (UNQ253) protein sequence SEQ ID NO:33 - Homo
(1003 aa) [1 seg]
Score = 5247 (2025 bits), Expect = 0.0
Identities = 1003/1003 (100%), Positives = 1003/1003 (100%), at 1,1-
1003,1003

DNA35680 1
MSQFEMDTYAKSHDLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLE

P_AAB65162 1
MSQFEMDTYAKSHDLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLE

DNA35680 61
GLRYTAVLKQQTQHSMLLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLK

P_AAB65162 61
GLRYTAVLKQQTQHSMLLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLK

DNA35680 121
LVPNHFFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDEL

P_AAB65162 121
LVPNHFFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDEL

DNA35680 181
AELETPEAAELDEQREKLVLSAECQLVTVVAVVPGLLEVTTQNVYFYDGSTERVETEEG

P_AAB65162 181
AELETPEAAELDEQREKLVLSAECQLVTVVAVVPGLLEVTTQNVYFYDGSTERVETEEG

DNA35680 241
IGYDFRRPLAQLEVLHRRFNLRSALELFFIDQANYFLNFPCKVGTTVPVSSPSQTPRPQ

P_AAB65162 241
IGYDFRRPLAQLEVLHRRFNLRSALELFFIDQANYFLNFPCKVGTTVPVSSPSQTPRPQ

DNA35680 301
PGPIPPHTQVRNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQ

BLAST RESULTS B-1

P_AAB65162 301
PGPIPPHTQVRNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQ

DNA35680 361
LNTIAGRTYNDLSQYPVFPWVLQDYVSPTLDLSNPAVFRDLSKPIGVVNPkHAQLVREKY

P_AAB65162 361
LNTIAGRTYNDLSQYPVFPWVLQDYVSPTLDLSNPAVFRDLSKPIGVVNPkHAQLVREKY

DNA35680 421
ESFEDPAGTIDKFHYGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAA

P_AAB65162 421
ESFEDPAGTIDKFHYGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAA

DNA35680 481
WQARLESPADVKELIPEFFYFPDFLENQNGFDLGCLQLTNEKVGDVVLPPWASSPEDFIQ

P_AAB65162 481
WQARLESPADVKELIPEFFYFPDFLENQNGFDLGCLQLTNEKVGDVVLPPWASSPEDFIQ

DNA35680 541
QHRQALESEYVSAHLHEWIDLIFGYKQRGPAEEEEALNVFYCTYEGAVDLHDHVTDERERK

P_AAB65162 541
QHRQALESEYVSAHLHEWIDLIFGYKQRGPAEEEEALNVFYCTYEGAVDLHDHVTDERERK

DNA35680 601
ALEGIISNFGQTPCQLLKEPHPTRLSAEEAAHRLARLDTNPSIFQHLDELKAFFAEVTV

P_AAB65162 601
ALEGIISNFGQTPCQLLKEPHPTRLSAEEAAHRLARLDTNPSIFQHLDELKAFFAEVTV

DNA35680 661
SASGLLGTHSWLPYDRNISNYFSFSKDPTMGSHKTQRLLSGPWVPGSGVSGQALAVAPDG

P_AAB65162 661
SASGLLGTHSWLPYDRNISNYFSFSKDPTMGSHKTQRLLSGPWVPGSGVSGQALAVAPDG

DNA35680 721
KLLFSGGHWGSLRVTALPRGKLLSQLSCHLDVVTCLALDTCGIY LISGSRDTCMVWRL

P_AAB65162 721
KLLFSGGHWGSLRVTALPRGKLLSQLSCHLDVVTCLALDTCGIY LISGSRDTCMVWRL

DNA35680 781
LHQGGLSVGLAPKPVQVLYGHGAAVSCVAISTELDMVSGSEDGTVIIHTVRRGQFVAAL

P_AAB65162 781
LHQGGLSVGLAPKPVQVLYGHGAAVSCVAISTELDMVSGSEDGTVIIHTVRRGQFVAAL

BLAST RESULTS B-2

DNA35680 841
RPLGATFPGPFIHFLALGSEGQIVVQSSAWERPGAQVTYSLHLYSVNGKLRASLPLAEQPT

P_AAB65162 841
RPLGATFPGPFIHFLALGSEGQIVVQSSAWERPGAQVTYSLHLYSVNGKLRASLPLAEQPT

DNA35680 901
ALVTEDFVLLGTAQCALHILQLNTLLPAAPPLPMKVAIRSVAVTKERSHVLVGLEDGKL

P_AAB65162 901
ALVTEDFVLLGTAQCALHILQLNTLLPAAPPLPMKVAIRSVAVTKERSHVLVGLEDGKL

DNA35680 961 IVVVGQPSSEVRSSQFARKLWRSSRRISQVSSGETEYNPTAR

P_AAB65162 961 IVVVGQPSSEVRSSQFARKLWRSSRRISQVSSGETEYNPTAR

>2 P_AAB24058 Human PRO290 protein sequence SEQ ID NO:7 - Homo sapiens.
(1003 aa) [1 seg]
Score = 5247 (2025 bits), Expect = 0.0
Identities = 1003/1003 (100%), Positives = 1003/1003 (100%), at 1,1-
1003,1003

DNA35680 1
MSQFEMDTYAKSHDLMSGFWNACYDMLSSGQRRQWERAQSRRAFQELVLEPAQRRARLE

P_AAB24058 1
MSQFEMDTYAKSHDLMSGFWNACYDMLSSGQRRQWERAQSRRAFQELVLEPAQRRARLE

DNA35680 61
GLRYTAVLKQQTQHSMLLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLK

P_AAB24058 61
GLRYTAVLKQQTQHSMLLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLK

DNA35680 121
LVPNHFFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDEL

P_AAB24058 121
LVPNHFFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDEL

DNA35680 181
AELETMPMAELDEQREKLVLSAECQLVTVVAVVPGLLEVTTQNVYFYDGSTERVETEEG

P_AAB24058 181
AELETMPMAELDEQREKLVLSAECQLVTVVAVVPGLLEVTTQNVYFYDGSTERVETEEG

DNA35680 241
IGYDFRRPLAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQ

P_AAB24058 241
IGYDFRRPLAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQ

DNA35680 301
PGPIPPHTQVRNQVYSWLLRLRPPSQGYLSSRSQPQEMLRASGLTQKWVQREISNFEYLMQ

BLAST RESULTS B-3

P_AAB24058 301
PGPIPPHTQVRNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQ

DNA35680 361
LNTIAGRTYNDLSQYPVFPWVLQDYVSPTLDLSNPAVFRDLSKPIGVNPKHAQLVREKY

P_AAB24058 361
LNTIAGRTYNDLSQYPVFPWVLQDYVSPTLDLSNPAVFRDLSKPIGVNPKHAQLVREKY

DNA35680 421
ESFEDPAGTIDKFHYGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAA

P_AAB24058 421
ESFEDPAGTIDKFHYGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAA

DNA35680 481
WQARLESPADVKEIPEFFYFPDFLENQNGFDLGCLQLTNEKVGDVVLPWASSPEDFIQ

P_AAB24058 481
WQARLESPADVKEIPEFFYFPDFLENQNGFDLGCLQLTNEKVGDVVLPWASSPEDFIQ

DNA35680 541
QHRQALESEYVSAHLHEWIDLIFGYKQRGPAEEALNVFYCYTYEGAVDLHDVTDERERK

P_AAB24058 541
QHRQALESEYVSAHLHEWIDLIFGYKQRGPAEEALNVFYCYTYEGAVDLHDVTDERERK

DNA35680 601
ALEGIISNFGQTPCQLLKEPHPTRLSAEEAAHRLARLDTNSPSIFQHLDELKAFFAEVTV

P_AAB24058 601
ALEGIISNFGQTPCQLLKEPHPTRLSAEEAAHRLARLDTNSPSIFQHLDELKAFFAEVTV

DNA35680 661
SASGLLGTHSWLPYDRNISNYFSFSKDPTMGSHKTQRLLSGPWVPGSGVSGQALAVAPDG

P_AAB24058 661
SASGLLGTHSWLPYDRNISNYFSFSKDPTMGSHKTQRLLSGPWVPGSGVSGQALAVAPDG

DNA35680 721
KLLFSGGHWGSLRVTALPRGKLLSQLSCHLDVVTCLALDTCGIY LISGSRD TTCMVWRL

P_AAB24058 721
KLLFSGGHWGSLRVTALPRGKLLSQLSCHLDVVTCLALDTCGIY LISGSRD TTCMVWRL

DNA35680 781
LHQGGLSVGLAPKPVQVLYGHGA AVSCVAISTELDMAVSGSEDGTVIIHTVRRGQFVAAL

P_AAB24058 781
LHQGGLSVGLAPKPVQVLYGHGA AVSCVAISTELDMAVSGSEDGTVIIHTVRRGQFVAAL

BLAST RESULTS B-A

DNA35680 841
RPLGATFPGPIFHLALGSEGQIVVQSSAWERPGAQVTYSLHLYSVNGKLRASLPLAEQPT

P_AAB24058 841
RPLGATFPGPIFHLALGSEGQIVVQSSAWERPGAQVTYSLHLYSVNGKLRASLPLAEQPT

DNA35680 901
ALTVTEDFVLLGTAQCALHILQLNTLLPAAPPLPMKVAIRSVAVTKERSHVLVGLEDGKL

P_AAB24058 901
ALTVTEDFVLLGTAQCALHILQLNTLLPAAPPLPMKVAIRSVAVTKERSHVLVGLEDGKL

DNA35680 961 IVVVAGQPSEVRSSQFARKLWRSSRRISQVSSGETEYNPTAR

P_AAB24058 961 IVVVAGQPSEVRSSQFARKLWRSSRRISQVSSGETEYNPTAR

>3 P_AAY66639 Membrane-bound protein PRO290 - Homo sapiens. (1004 aa) [1
seg]

Score = 5235 (2021 bits), Expect = 0.0
Identities = 1003/1004 (99%), Positives = 1003/1004 (99%), Gaps =
1/1004 (0%), at 1,1-1003,1004

DNA35680 1
MSQFEMDTYAKSHDLMSGFWNACYDMLSSGQRRQWERAQSRRAFQELVLEPAQRRARLE

P_AAY66639 1
MSQFEMDTYAKSHDLMSGFWNACYDMLSSGQRRQWERAQSRRAFQELVLEPAQRRARLE

DNA35680 61
GLRYTAVLKQQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLK

P_AAY66639 61
GLRYTAVLKQQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLK

DNA35680 121
LVPNHHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDEL

P_AAY66639 121
LVPNHHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDEL

DNA35680 181
AELETPMEEAELDEQREKLVLSAECQLTVVAVVPGLLEVTTQNVYFYDGSTERVETEEG

P_AAY66639 181
AELETPMEEAELDEQREKLVLSAECQLTVVAVVPGLLEVTTQNVYFYDGSTERVETEEG

DNA35680 241
IGYDFRRPLAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQ

P_AAY66639 241
IGYDFRRPLAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQ

DNA35680 301
PGPIPPHTQVRNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQ

Blast Results B-5

P_AAY66639 301
PGPIPPHTQVRNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQ

DNA35680 361
LNTIAGRTYNDLSQYPVFPWVLQDYVSPTLDLSNPAVFRDLSKPIGVVNPKAQLVREKY

P_AAY66639 361
LNTIAGRTYNDLSQYPVFPWVLQDYVSPTLDLSNPAVFRDLSKPIGVVNPKAQLVREKY

DNA35680 421
ESFEDPAGTIDKFHYGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAA

P_AAY66639 421
ESFEDPAGTIDKFHYGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAA

DNA35680 481
WQARLESPADVKEIPEFFYFPDFLENQNGFDLGCLQLTNEKVGDVVLPPWASSPEDFIQ

P_AAY66639 481
WQARLESPADVKEIPEFFYFPDFLENQNGFDLGCLQLTNEKVGDVVLPPWASSPEDFIQ

DNA35680 541
QHRQALESEYVSAHLHEWIDLIFGYKQRGPAEEALNVFYYCTYEGAVDLDHVTDERERK

P_AAY66639 541
QHRQALESEYVSAHLHEWIDLIFGYKQRGPAEEALNVFYYCTYEGAVDLDHVTDERERK

DNA35680 601
ALEGIISNFGQTPCQLLKEPHPTRLSAEEAAHRLARLDTNSPSIFQHLDELKAFFAEVTV

P_AAY66639 601
ALEGIISNFGQTPCQLLKEPHPTRLSAEEAAHRLARLDTNSPSIFQHLDELKAFFAEVTV

DNA35680 661
SASGLLGTHSWLPYDRNISNYFSFSKDPTMGSHKTQRLLSGPWVPGSGVSGQALAVAPDG

P_AAY66639 661
SASGLLGTHSWLPYDRNISNYFSFSKDPTMGSHKTQRLLSGPWVPGSGVSGQALAVAPDG

DNA35680 721
KLLFSGGHWGSLRVLTALPRGKLLSQLSCHLDVVTCLALDTCGIY LISGSRDTTCMVWRL

P_AAY66639 721
KLLFSGGHWGSLRVLTALPRGKLLSQLSCHLDVVTCLALDTCGIY LISGSRDTTCMVWRL

DNA35680 781
LHQGGLSVGLAPKPVQVLYGHGAAVSCVAISTELDMAVSGSEDGTVIIHTVRRGQFVAAL

P_AAY66639 781
LHQGGLSVGLAPKPVQVLYGHGAAVSCVAISTELDMAVSGSEDGTVIIHTVRRGQFVAAL

Blast Results B-6

DNA35680 841
RPLGATFPGPIFHLALGSEGQIVVQSSAWERPGAQVTYSLHLYSVNGKLRASLPLAEQPT

P_AAY66639 841
RPLGATFPGPIFHLALGSEGQIVVQSSAWERPGAQVTYSLHLYSVNGKLRASLPLAEQPT

DNA35680 901 ALTVTEDFVLLGTAQCALHI-
LQLNTLLPAAPPLPMKVAIRSVAVTKERSHVLVGLEDGK

P_AAY66639 901
ALTVTEDFVLLGTAQCALHILLQLNTLLPAAPPLPMKVAIRSVAVTKERSHVLVGLEDGK

DNA35680 960 LIVVVAGQPSEVRSSQFARKLWRSSRRISQVSSGETEYNPTAR

P_AAY66639 961 LIVVVAGQPSEVRSSQFARKLWRSSRRISQVSSGETEYNPTAR

>4 P_AAB80418 Gene #4 associated peptide #1 - Homo sapiens. (1041 aa) [1
seg]

Score = 5206 (2009 bits), Expect = 0.0
Identities = 1003/1033 (97%), Positives = 1003/1033 (97%), Gaps =
30/1033 (2%), at 1,9-1003,1041

DNA35680 1
MSQFEMDTYAKSHDLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLE

P_AAB80418 9
MSQFEMDTYAKSHDLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLE

DNA35680 61
GLRYTAVLKQQTQHSMLLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLK

P_AAB80418 69
GLRYTAVLKQQTQHSMLLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLK

DNA35680 121
LVPNHFFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDEL

P_AAB80418 129
LVPNHFFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDEL

DNA35680 181
AELETPEAAELDEQREKLVLSAECQLVTVVAVVPGLLEVTTQNVYFYDGSTERVETEEG

P_AAB80418 189
AELETPEAAELDEQREKLVLSAECQLVTVVAVVPGLLEVTTQNVYFYDGSTERVETEEG

DNA35680 241
IGYDFRRPLAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTTPVSSPSQTPRPQ

P_AAB80418 249
IGYDFRRPLAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTTPVSSPSQTPRPQ

DNA35680 301
PGPIPPHTQVRNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQ

BLAST RESULTS B-7

P_AAB80418 309
PGPIPPHTQVRNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQ

DNA35680 361
LNTIAGRTYNDLSQYPVFPWVLQDYVSPTLDLSNPAVFRDLSKPIGVVNPKHAQLVREKY

P_AAB80418 369
LNTIAGRTYNDLSQYPVFPWVLQDYVSPTLDLSNPAVFRDLSKPIGVVNPKHAQLVREKY

DNA35680 421
ESFEDPAGTIDKFHYGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAA

P_AAB80418 429
ESFEDPAGTIDKFHYGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAA

DNA35680 481
WQARLESPADVKEIPEFFYFPDFLENQNGFDLGCLQLTNEKVGDVVLPPWASSPEDFIQ

P_AAB80418 489
WQARLESPADVKEIPEFFYFPDFLENQNGFDLGCLQLTNEKVGDVVLPPWASSPEDFIQ

DNA35680 541
QHRQALESEYVSAHLHEWIDLIFGYKQRGPAEEALNVFYYCTYEGAVDLDHVTDERERK

P_AAB80418 549
QHRQALESEYVSAHLHEWIDLIFGYKQRGPAEEALNVFYYCTYEGAVDLDHVTDERERK

DNA35680 601
ALEGIISNFGQTPCQLLKEPHPTRLSAEEAAHRLARLDTNSPSIFQHLDELKAFFAE---

P_AAB80418 609
ALEGIISNFGQTPCQLLKEPHPTRLSAEEAAHRLARLDTNSPSIFQHLDELKAFFAEVVS

DNA35680 658 -----
VTVSASGLLGTHSWLPYDRNISNYFSFSKDPTM

P_AAB80418 669
DGVFLVLALVPHRQPHSFITQGSPDLLVTVSASGLLGTHSWLPYDRNISNYFSFSKDPTM

DNA35680 691
GSHKTQRLLSGPWVPGSGVSGQALAVAPDGKLLFSGGHWGSLRVLTALPRGKLLSQLSCH

P_AAB80418 729
GSHKTQRLLSGPWVPGSGVSGQALAVAPDGKLLFSGGHWGSLRVLTALPRGKLLSQLSCH

DNA35680 751
LDVVTCLALDTCGIYLISGSRDTCMVWRLHQQGLSVGLAPKPVQVLYGHGAAVSCVAI

P_AAB80418 789
LDVVTCLALDTCGIYLISGSRDTCMVWRLHQQGLSVGLAPKPVQVLYGHGAAVSCVAI

BLAST RESULTS B-B

BLAST RESULTS B-9

DNA35680 811
STELDMAVSGSEDGTVIIHTVRRGQFVAALRPLGATFPGPFIHFLALGSEQIIVVQSSAWE

P_AAB80418 849
STELDMAVSGSEDGTVIIHTVRRGQFVAALRPLGATFPGPFIHFLALGSEQIIVVQSSAWE

DNA35680 871
RPGAQVTYSLHLYSVNGKLRLASLPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA

P_AAB80418 909
RPGAQVTYSLHLYSVNGKLRLASLPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA

DNA35680 931
PPLPMKVAIRSVAVTKERSHVLVGLEDGKLIVVAGQPSEVRSSQFARKLWRSSRRISQV

P_AAB80418 969
PPLPMKVAIRSVAVTKERSHVLVGLEDGKLIVVAGQPSEVRSSQFARKLWRSSRRISQV

DNA35680 991 SSGETEYNPTEAR

P_AAB80418 1029 SSGETEYNPTEAR

>5 P_AAB80374 Secreted protein encoded by gene #4 - Homo sapiens. (957
aa) [1 seg]

Score = 4810 (1857 bits), Expect = 0.0

Identities = 927/957 (96%), Positives = 927/957 (96%), Gaps = 30/957
(3%), at 77,1-1003,957

DNA35680 77
MALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLKLVNHHFDPHLEASAL

P_AAB80374 1
MALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLKLVNHHFDPHLEASAL

DNA35680 137
RDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELAELETPMEAAELDEQR

P_AAB80374 61
RDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELAELETPMEAAELDEQR

DNA35680 197
EKLVLSAECQLVTVVAVVPGLETTQNVYFYDGSSTERVETEEGIGYDFRRPLAQLREXH

P_AAB80374 121
EKLVLSAECQLVTVVAVVPGLETTQNVYFYDGSSTERVETEEGIGYDFRRPLAQLREXH

DNA35680 257
LRRFNLRRSALELFFIDQANYFLNFPCKVGTTVPVSSPSQTPRPQGPPIPPHTQVRNQVYS

P_AAB80374 181
LRRFNLRRSALELFFIDQANYFLNFPCKVGTTVPVSSPSQTPRPQGPPIPPHTQVRNQVYS

DNA35680 317
WLLRLRPSSQGYLSSRSPOEMLRASGLTQKWVQREISNFEYLMQLNTIAGRITYNDLSQYP

P_AAB80374 241
WLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQLNTIAGRITYNDLSQYP

DNA35680 377
VFPWVLQDYVSPTLDLSNPAVFRDLSKPIGVVNPKHAQLVREKYESFEDPAGTIDKFHYG

P_AAB80374 301
VFPWVLQDYVSPTLDLSNPAVFRDLSKPIGVVNPKHAQLVREKYESFEDPAGTIDKFHYG

DNA35680 437
THYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAAWQARLESPADV KELIP

P_AAB80374 361
THYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAAWQARLESPADV KELIP

DNA35680 497
EFFYFPDFLENQNGFDLGCQLTNEKVGDVVLPWASSPEDFIQQHRQALESEYVSAHLH

P_AAB80374 421
EFFYFPDFLENQNGFDLGCQLTNEKVGDVVLPWASSPEDFIQQHRQALESEYVSAHLH

DNA35680 557
EWIDLIFGYKQRGPAEEALNVFYYCTYEGAVDL DHVTDERERKALEGIISNFGQTPCQL

P_AAB80374 481
EWIDLIFGYKQRGPAEEALNVFYYCTYEGAVDL DHVTDERERKALEGIISNFGQTPCQL

DNA35680 617
LKEPHPTRLSAEEAAHRLARLDTNSPSIFQHLDLDELKAFFAE-----

P_AAB80374 541
LKEPHPTRLSAEEAAHRLARLDTNSPSIFQHLDLDELKAFFAEVVS DGVPLVLALVPHRQPH

DNA35680 658 -----
VTVSASGLLGTHSWLPYDRNISNYFSFSKDPTMGSHKTQRLLSGPWVPG

P_AAB80374 601
SFITQGPDLLVTVSASGLLGTHSWLPYDRNISNYFSFSKDPTMGSHKTQRLLSGPWVPG

DNA35680 707
SGVSGQALAVAPDGKLLFSGGHWGSLRV TALPRGKLLSQLSCHLDVVTCLALDTCGIYL

P_AAB80374 661
SGVSGQALAVAPDGKLLFSGGHWGSLRV TALPRGKLLSQLSCHLDVVTCLALDTCGIYL

DNA35680 767
ISGSRDTTCMVWRL LHQGGLSVGLAPKPVQVLYGHGA AVSCVAISTELDM AVSGSEDGTV

P_AAB80374 721
ISGSRDTTCMVWRL LHQGGLSVGLAPKPVQVLYGHGA AVSCVAISTELDM AVSGSEDGTV

DNA35680 827

Blast Results B-10

IIHTVRRGQFVAALRPLGATFPGPFIHFLALGSEGQIVVQSSAWERPGAQVTYSLHLYSVN

P_AAB80374 781

IIHTVRRGQFVAALRPLGATFPGPFIHFLALGSEGQIVVQSSAWERPGAQVTYSLHLYSVN

DNA35680 887

GKLRASLPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAAPPLPMKVAIRSVAVTK

P_AAB80374 841

GKLRASLPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAAPPLPMKVAIRSVAVTK

DNA35680 947

ERSHVLVGLEDGKLIVVVAGQPSEVRSSQFARKLWRSSRRISQVSSGETEYNPTAR

P_AAB80374 901

ERSHVLVGLEDGKLIVVVAGQPSEVRSSQFARKLWRSSRRISQVSSGETEYNPTAR

Blast Results B-11